

Fig. 1B

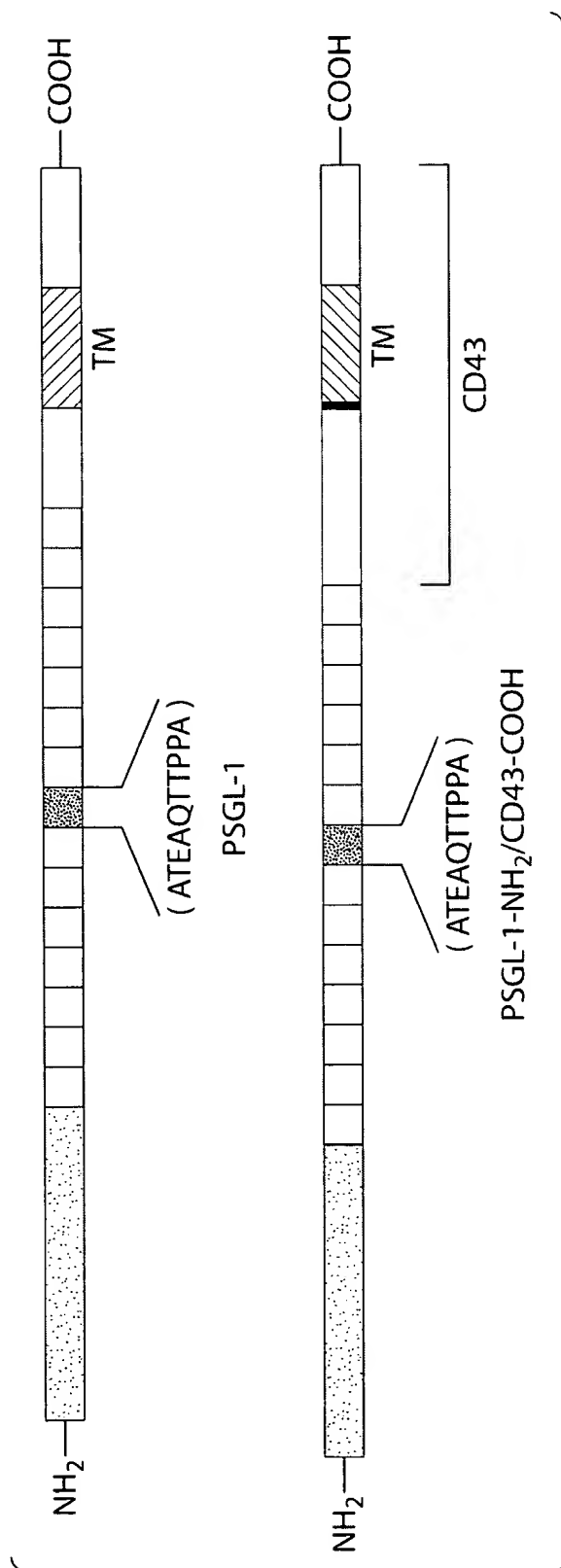


Fig. 2A

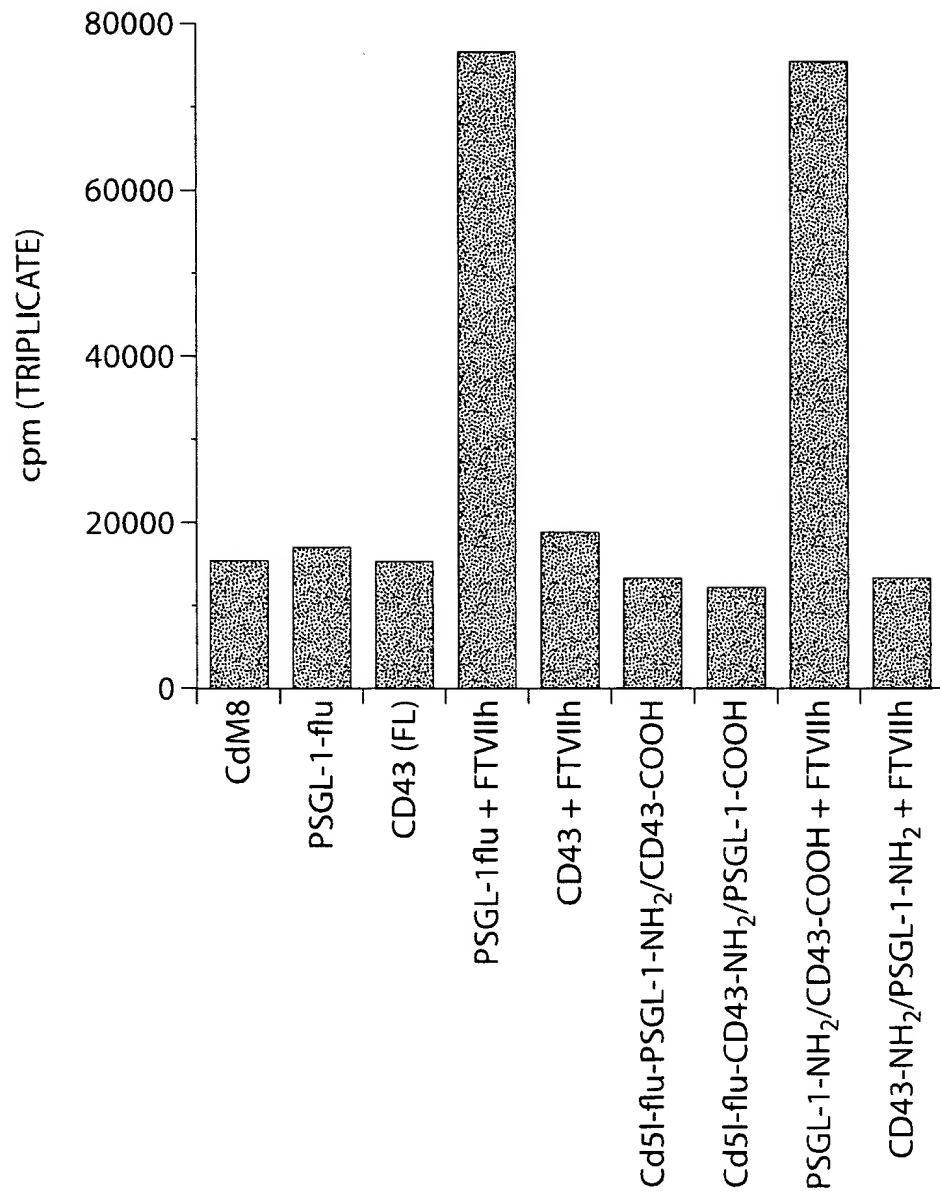


Fig. 2B

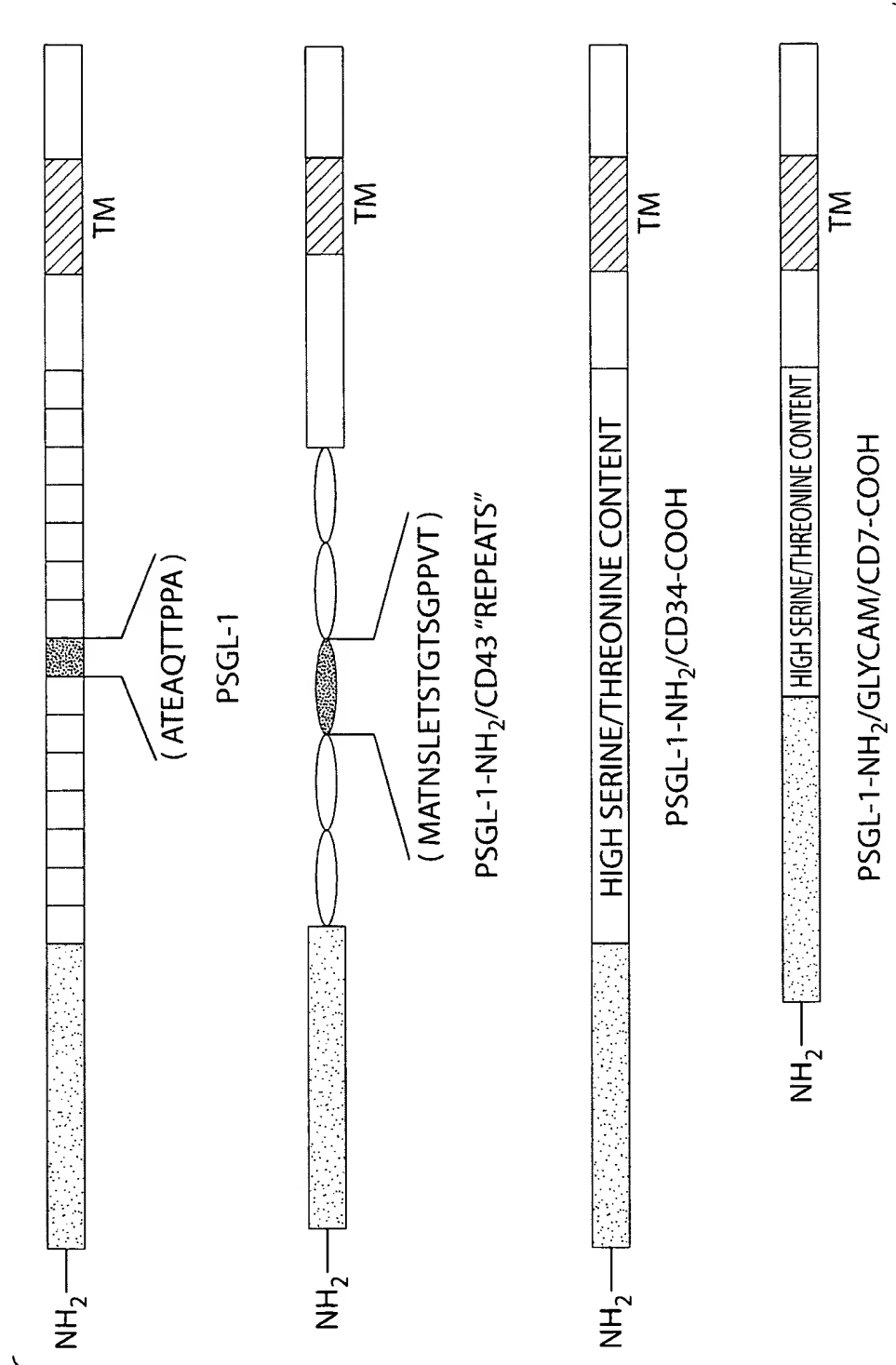


Fig. 3A

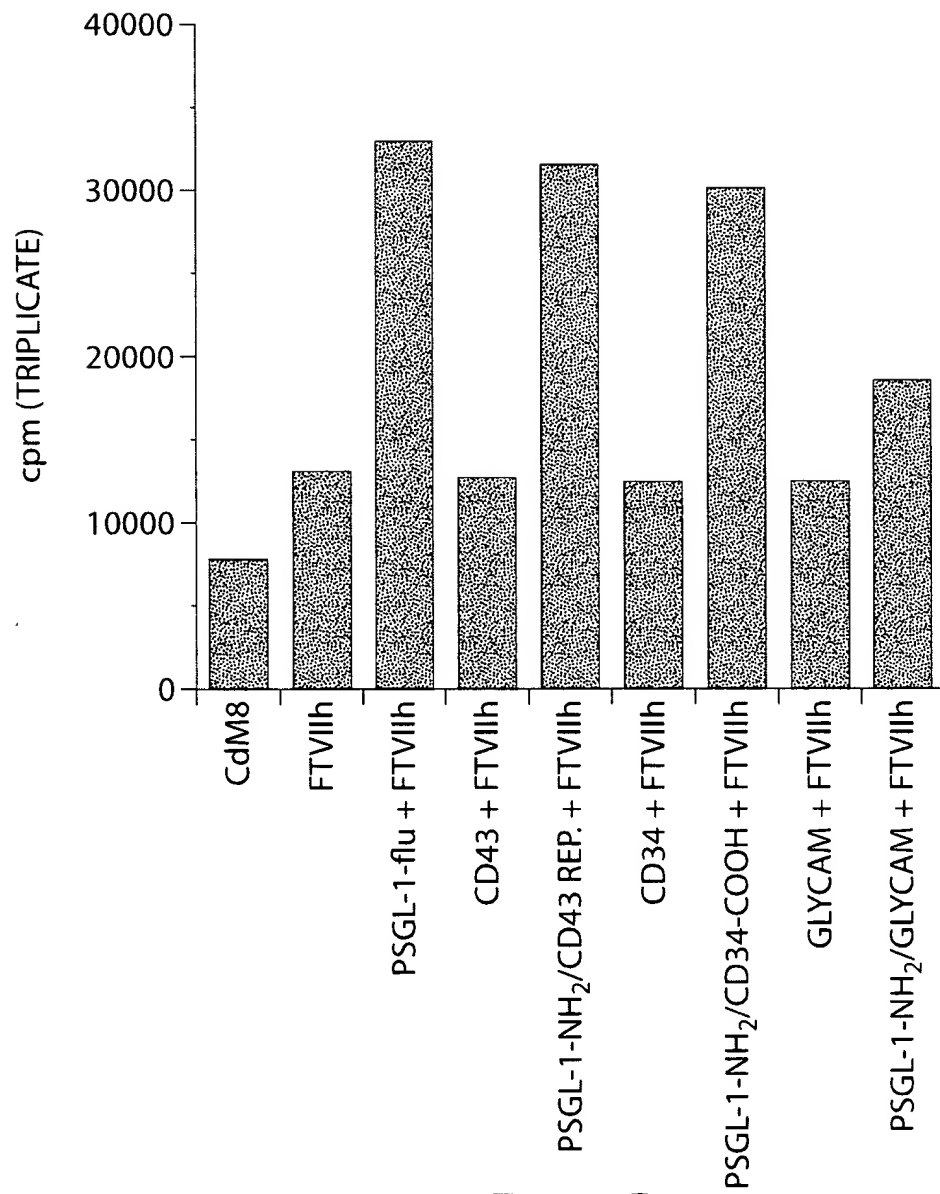


Fig. 3B

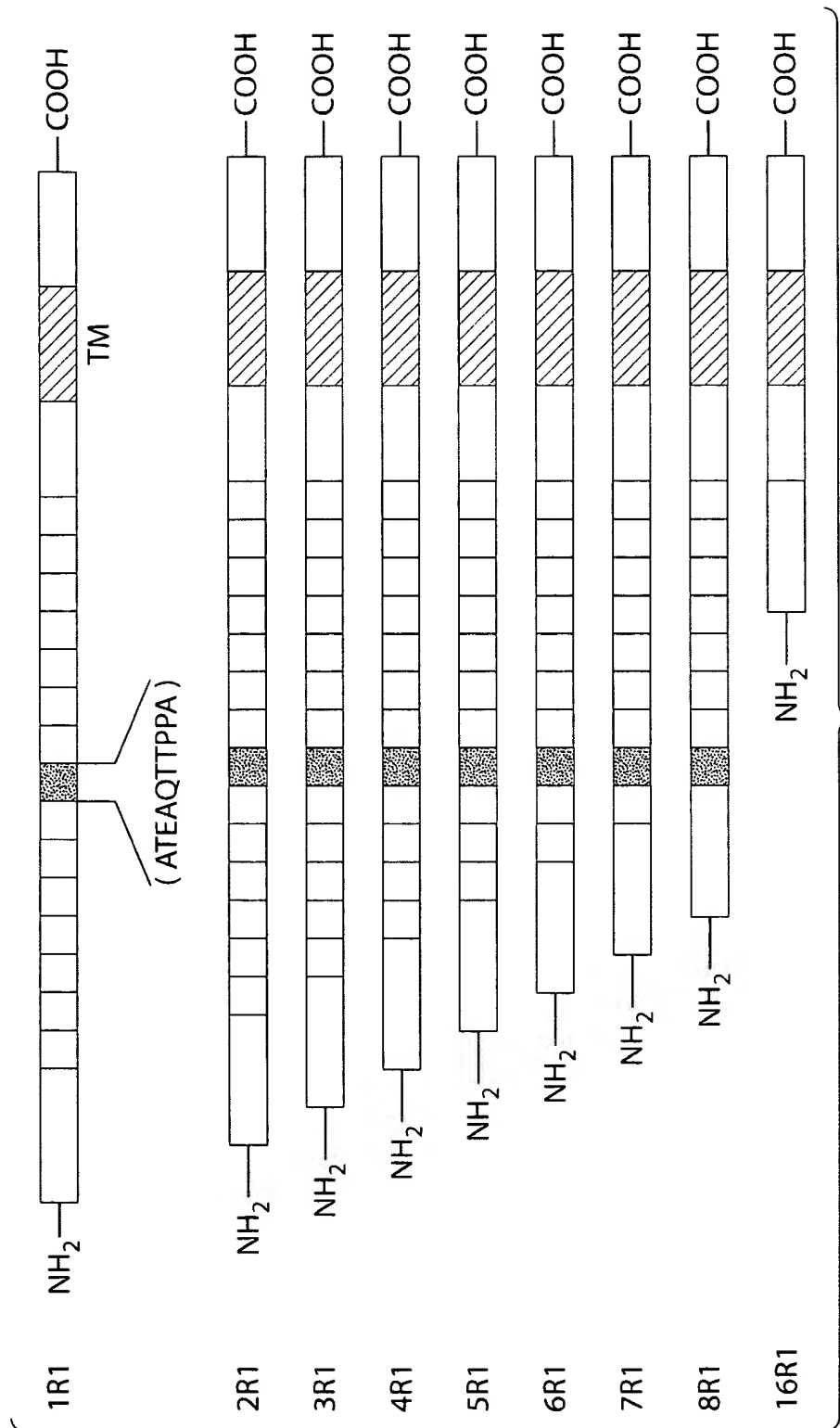


Fig. 4A

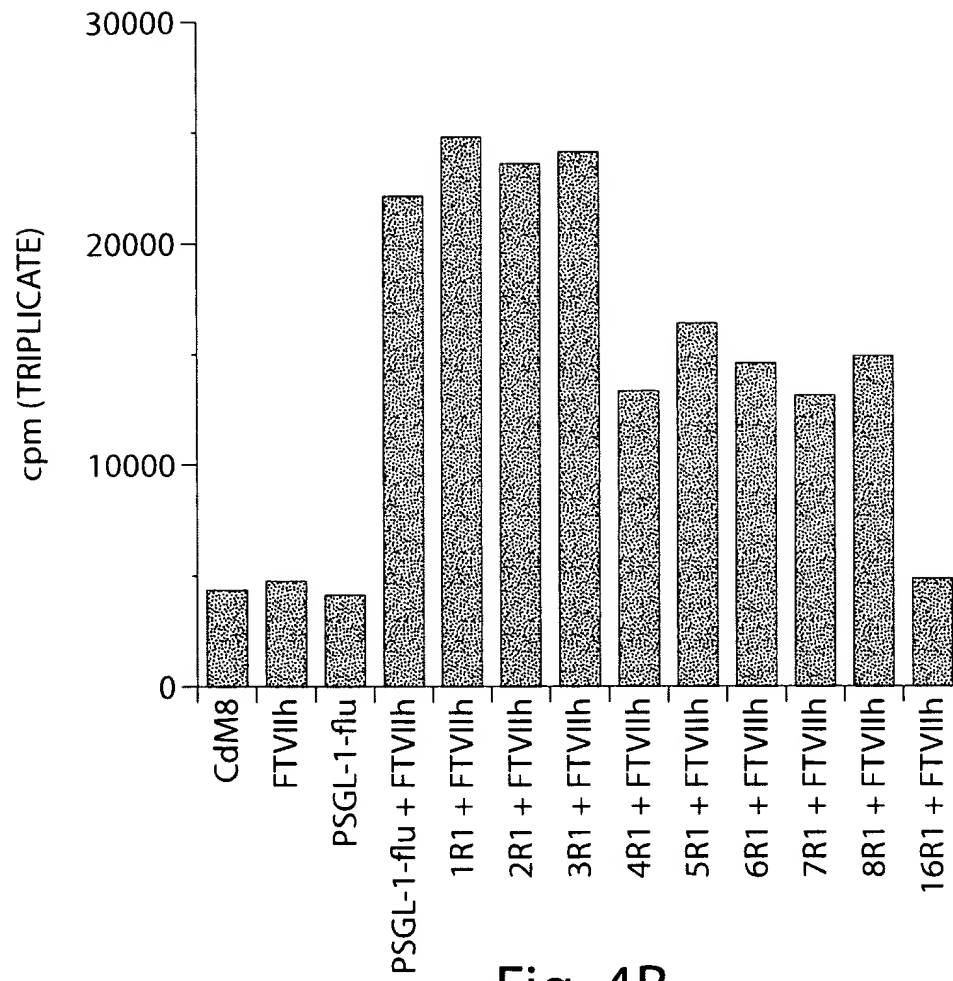


Fig. 4B

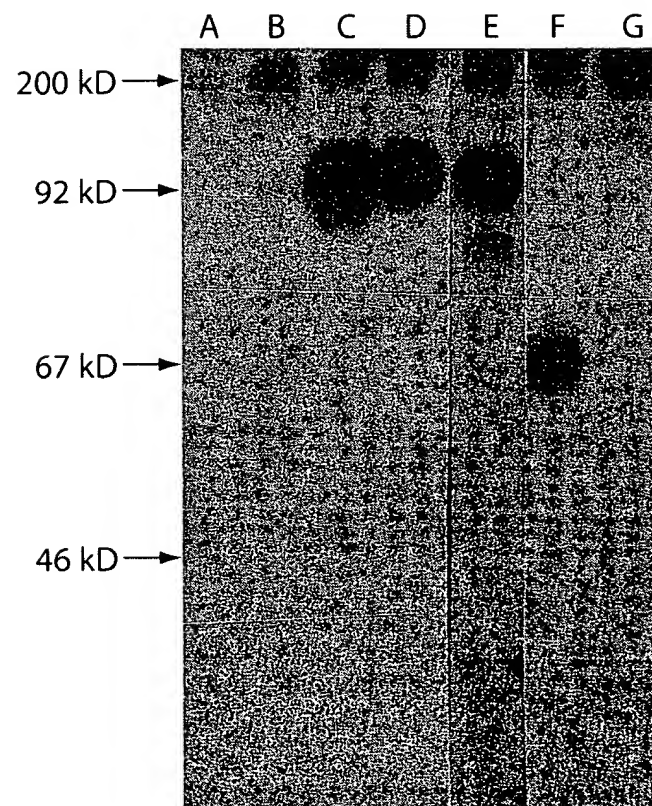


Fig. 5

10/26

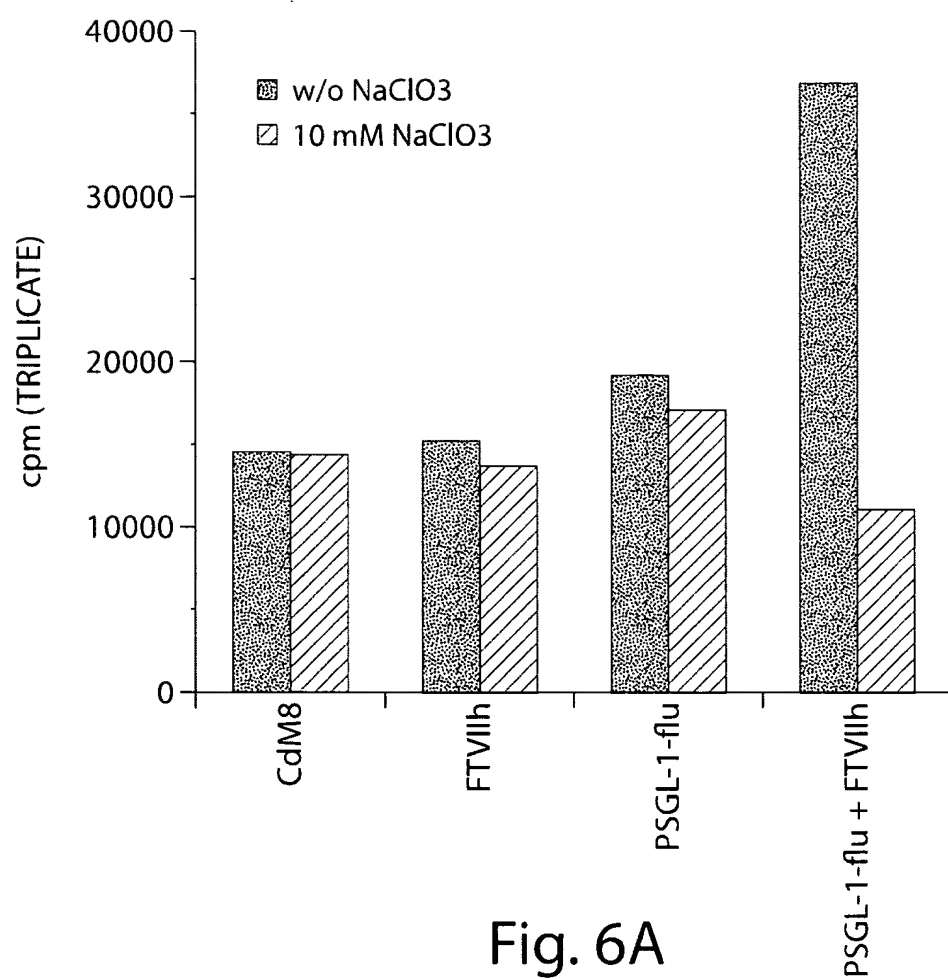


Fig. 6A

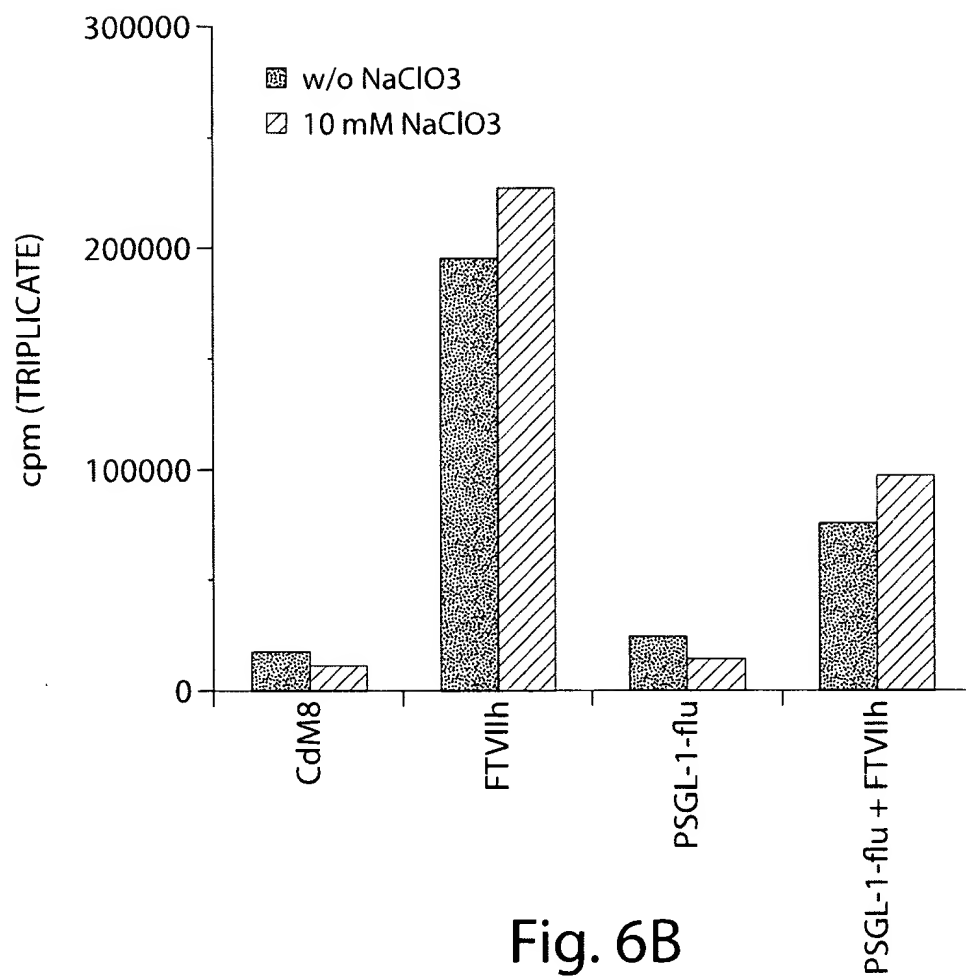


Fig. 6B

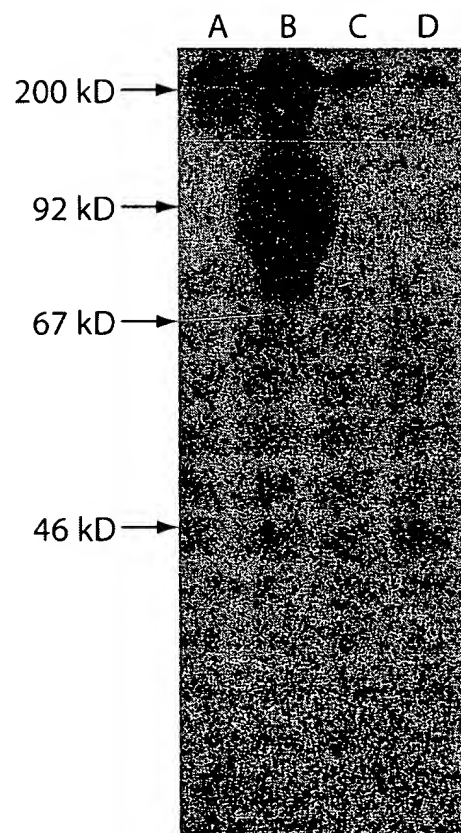


Fig. 7

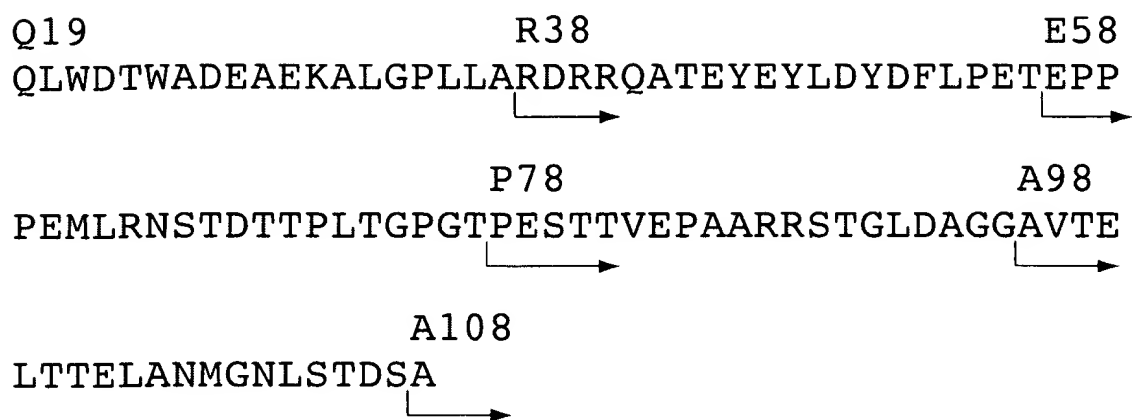


Fig. 8A

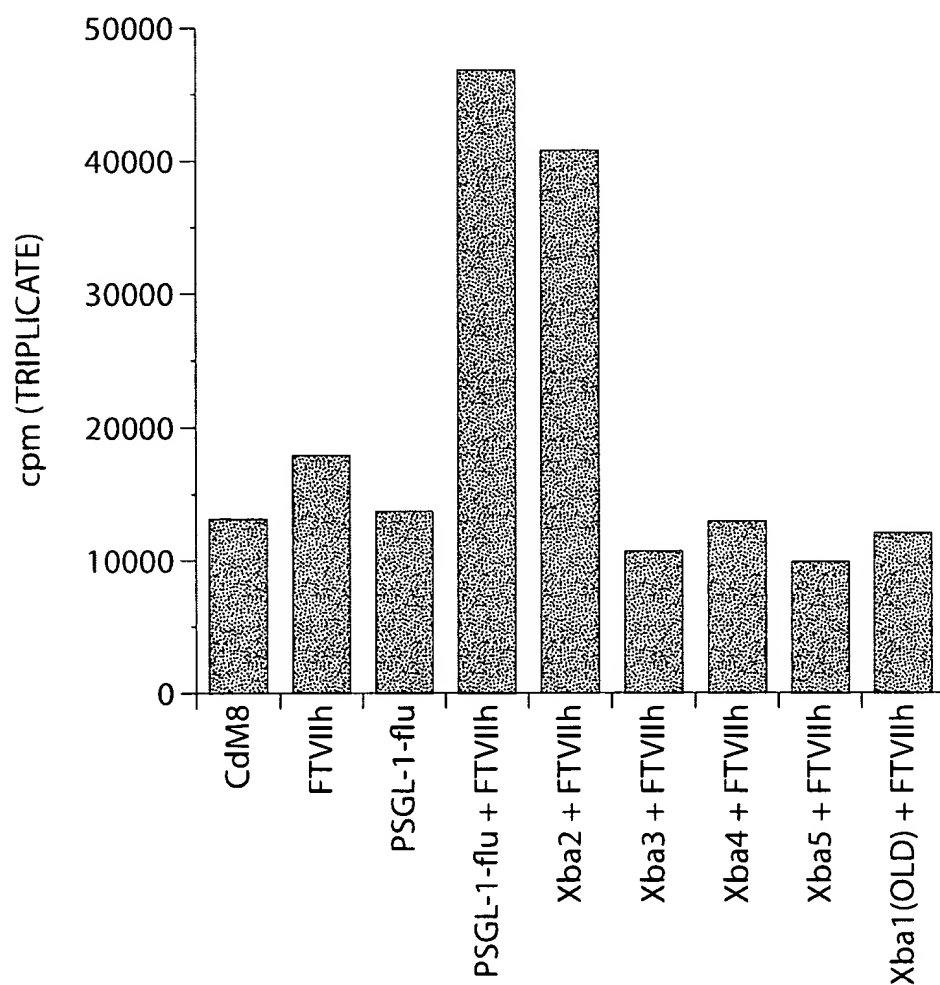


Fig. 8B

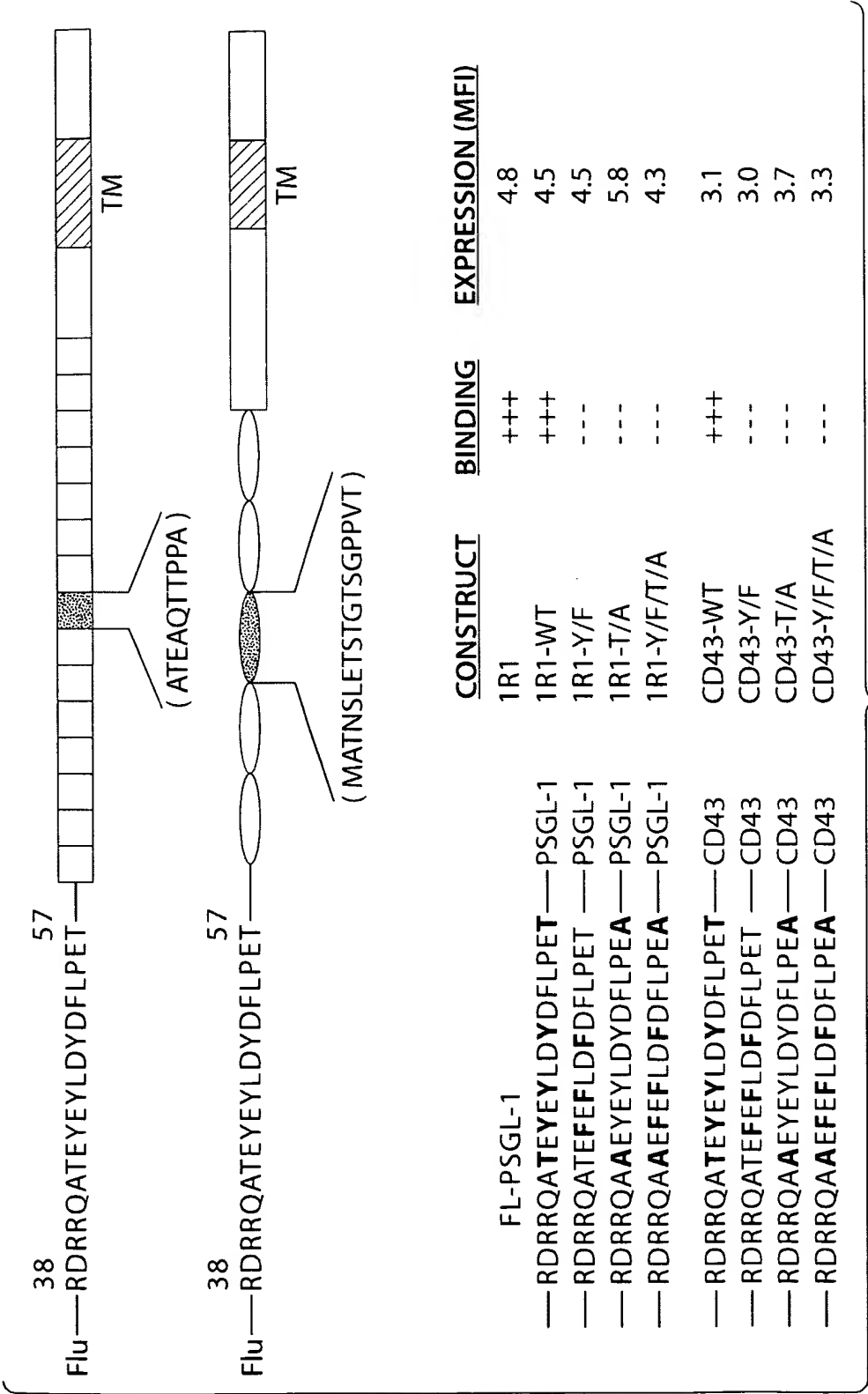


Fig. 9A

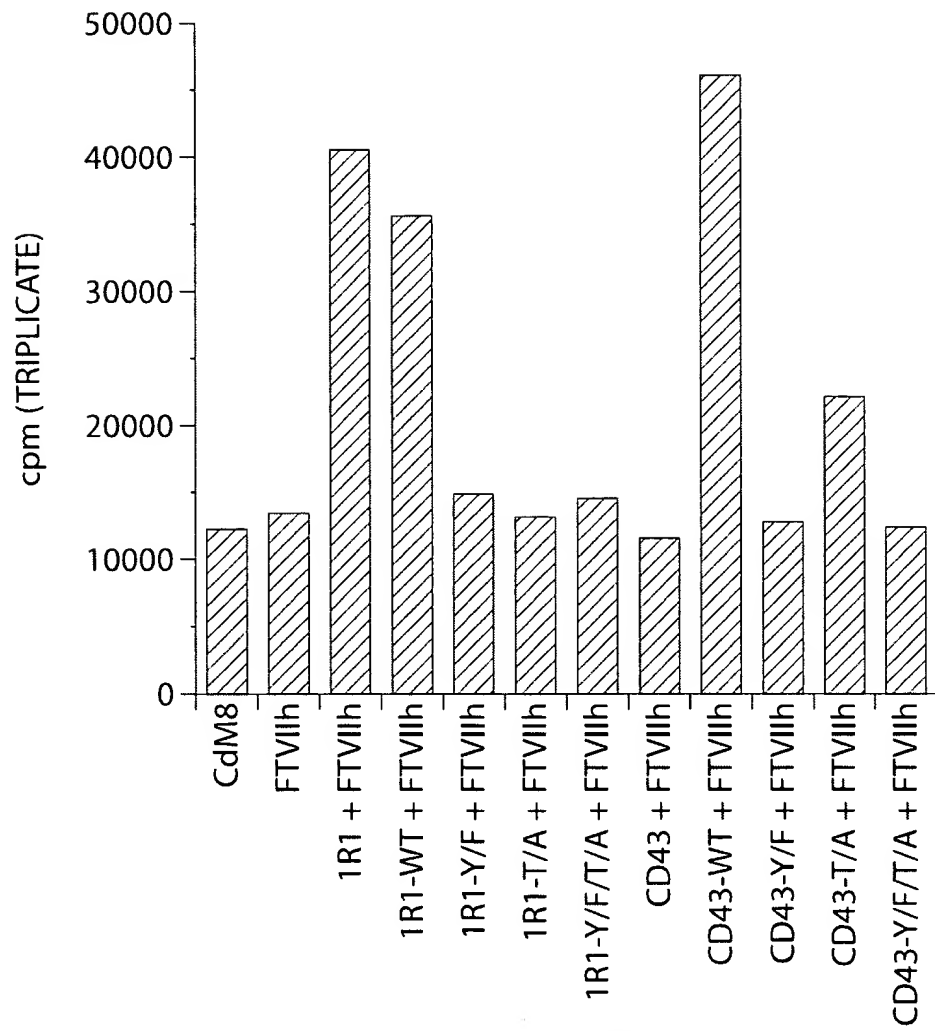


Fig. 9B

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AAGCTTACCACCATGGACTGGACCTGGAGGTTCTCTTCTTTGTGGTGGCAGCAGCTACA
1  -----+-----+-----+-----+-----+-----+ 60
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K L T T M D W T W R F L F F V V A A A T -

GGTGTCCAGTCCCAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCC
61  -----+-----+-----+-----+-----+-----+ 120
CCACAGGTGAGGGTCCACGTGACACGTGACACCCGACTCCACTTCTTCGGACCCAGG

G V Q S Q V Q L V Q S G A E V K K P G S -

TCGGTGAAGGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGG
121 -----+-----+-----+-----+-----+-----+ 180
AGCCACTTCCAGAGGACGTTCGAAGACCTCCGTGGAAGTCGTCGATACGATAGTCGACC

S V K V S C K A S G G T F S S Y A I S W -

GTGCGACAGGCCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGT
181 -----+-----+-----+-----+-----+-----+ 240
CACGCTGTCCGGGGACCTGTTCCCGAACTCACCTACCCTCCCTAGTAGGGATAGAAACCA

V R Q A P G Q G L E W M G G I I P I F G +

ACAGCAAACCTACGCACAGAAGTTCCAGGGCAGAGTCACGATTACCGCGGACGAATCCACG
241 -----+-----+-----+-----+-----+-----+ 300
TGTCGTTTGATGCGTGTCTTCAAGGTCCCGTCTCAGTGCTAATGGCGCCTGCTTAGGTGC

T A N Y A Q K F Q G R V T I T A D E S T -

AGCACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT
301 -----+-----+-----+-----+-----+-----+ 360
TCGTGTCGGATGTACCTCGACTCGTCCGACTCTAGACTCCTGTGCCGGCACATAATGACA

S T A Y M E L S S L R S E D T A V Y Y C -

GCGAGAGATAATGGAGCGTATTGTAGTGGTGGTAGCTGCTACTCGGGCTGGTTCGACCCC
361 -----+-----+-----+-----+-----+-----+ 420
CGCTCTCTATTACCTCGCATAACATCACCACCATCGACGATGAGCCCGACCAAGCTGGGG

A R D N G A Y C S G G S C Y S G W F D P -

TGGGGCCAGGGAACCCTGGTCACCGTCTCTTCAGGTGAGTACTGAATTCTAGCTTTCTGG
421 -----+-----+-----+-----+-----+-----+ 480
ACCCCGGTCCCTTGGGACCAGTGGCAGAGAAGTCCACTCATGACTTAAGATCGAAAGACC

W G Q G T L V T V S S

```

Fig. 10A

GGCAGGCCAGGCCTGACCTTGGCTTTGGGGCAGGGAGGGGGCTAAGGTGAGGCAGGTGGC
 481 -----+-----+-----+-----+-----+-----+ 540
 CCGTCCGGTCCGGACTGGAACCGAAACCCCGTCCCTCCCCGATTCCACTCCGTCCACCG

 GCCAGCAGGTGCACACCCAATGCCCATGAGCCCAGACACTGGACGCTGAACCTCGCGGAC
 541 -----+-----+-----+-----+-----+-----+ 600
 CCGTTCGTCCACGTGTGGGTACGGGTACTCGGGTCTGTGACCTGCGACTTGGAGCGCCTG

 AGTTAAGAACCCAGGGGCCTCTGCGCCTGGGCCCAGCTCTGTCCCACACCGCGGTACAT
 601 -----+-----+-----+-----+-----+-----+ 660
 TCAATTCTTGGGTCCCCGGAGACGCGGACCCGGGTTCGAGACAGGGTGTGGCGCCAGTGTA

 GGCACCACCTCTCTTGCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCC
 661 -----+-----+-----+-----+-----+-----+ 720
 CCGTGGTGGAGAGAACGTTCGGAGGTGGTTCCCGGGTAGCCAGAAGGGGGACCGTGGGAGG

 A S T K G P S V F P L A P S -

 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC
 721 -----+-----+-----+-----+-----+-----+ 780
 AGGTTCTCGTGGAGACCCCCGTGTGCGCGGGACCCGACGGACCAGTTCCTGATGAAGGGG

 S K S T S G G T A A L G C L V K D Y F P -

 GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCG
 781 -----+-----+-----+-----+-----+-----+ 840
 CTTGGCCACTGCCACAGCACCTTGAGTCCGCGGGACTGGTTCGCCGCACGTGTGGAAGGGC

 E P V T V S W N S G A L T S G V H T F P -

 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC
 841 -----+-----+-----+-----+-----+-----+ 900
 CGACAGGATGTCAGGAGTCCTGAGATGAGGGAGTCGTGCGACCACTGGCACGGGAGGTGC

 A V L Q S S G L Y S L S S V V T V P S S -

 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
 901 -----+-----+-----+-----+-----+-----+ 960
 TCGAACCCGTGGGTCTGGATGTAGACGTTGCACTTAGTGTTCGGGTCGTTGTGGTTCCAC

 S L G T Q T Y I C N V N H K P S N T K V -

 GACAAGAAAGTTGGTGAGAGGCCAGCACAGGGAGGGAGGGTGTCTGCTGGAAGCAGGCTC
 961 -----+-----+-----+-----+-----+-----+ 1020
 CTGTTCTTTCAACCACTCTCCGGTTCGTGTCCCTCCCTCCACAGACGACCTTCGTCCGAG

 D K K V

Fig. 10B

1021 AGCGCTCCTGCCTGGACGCATCCCGGCTATGCAGCCCCAGTCCAGGGCAGCAAGGCAGGC 1080
 -----+-----+-----+-----+-----+-----+ 1080
 TCGCGAGGACGGACCTGCGTAGGGCCGATACGTCGGGGTCAGGTCCCGTCGTTCCGTCCG

 1081 CCCGTCTGCCTCTTCACCCGGAGCCTCTGCCCCCCCCACTCATGCTCAGGGAGAGGGTCT 1140
 -----+-----+-----+-----+-----+-----+ 1140
 GGGCAGACGGAGAAGTGGGCCTCGGAGACGGGCGGGGTGAGTACGAGTCCCTCTCCAGA

 1141 TCTGGCTTTTTTCCCAGGCTCTGGGCAGGCACAGGCTAGGTGCCCCCTAACCCAGGCCCTGC 1200
 -----+-----+-----+-----+-----+-----+ 1200
 AGACCGAAAAAGGGTCCGAGACCCGTCCGTGTCCGATCCACGGGGATTGGGTCCGGGACG

 1201 ACACAAAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCCGGGAGGACCCTGC 1260
 -----+-----+-----+-----+-----+-----+ 1260
 TGTGTTTCCCCGTCCACGACCCGAGTCTGGACGGTTCTCGGTATAGGCCCTCCTGGGACG

 1261 CCCTGACCTAAGCCCACCCCAAAGGCCAAACTCTCCACTCCCTCAGCTCGGACACCTTCT 1320
 -----+-----+-----+-----+-----+-----+ 1320
 GGGACTGGATTCCGGTGGGGTTTCCGGTTTGAGAGGTGAGGGAGTCGAGCCTGTGGAAGA

 1321 CTCCTCCCAGATTCCAGTAACTCCCAATCTTCTCTCTGCAGAGCCCAAATCTTGTGACAA 1380
 -----+-----+-----+-----+-----+-----+ 1380
 GAGGAGGGTCTAAGGTCATTGAGGGTTAGAAGAGAGACGTCTCGGGTTTAGAACACTGTT

 E P K S C D K -

 1381 AACTCACACATGCCCACCGTGCCCAGGTAAGCCAGCCCAGGCCTCGCCCTCCAGCTCAAG 1440
 -----+-----+-----+-----+-----+-----+ 1440
 TTGAGTGTGTACGGGTGGCAGGGTCCATTTCGGTCGGGTCCGGAGCGGGAGGTTCGAGTTC

 T H T C P P C P

 1441 GCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGGCCCCAGCCGGGTGCTGACA 1500
 -----+-----+-----+-----+-----+-----+ 1500
 CGCCCTGTCCACGGGATCTCATCGGACGTAGGTCCCTGTCCGGGGTCGGCCCACGACTGT

 1501 CGTCCACCTCCATCTCTTCCTCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCT 1560
 -----+-----+-----+-----+-----+-----+ 1560
 GCAGGTGGAGGTAGAGAAGGAGTCGTGGACTTGAGGACCCCCCTGGCAGTCAGAAGGAGA

 A P E L L G G P S V F L F -

Fig. 10C

1561 TCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACACATGCGTGG
 -----+-----+-----+-----+-----+-----+ 1620
 AGGGGGGTTTGGGTTCTGTGGGAGTACTAGAGGGCTGGGACTCCAGTGTACGCACC
 P P K P K D T L M I S R T P E V T C V V -

1621 TGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGG
 -----+-----+-----+-----+-----+-----+ 1680
 ACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCACCTGCCGCACC
 V D V S H E D P E V ^NK ^SF N W Y V D G V E -

1681 AGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGG
 -----+-----+-----+-----+-----+-----+ 1740
 TCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTGCATGGCCCACC
 V H N ^NA K T K P R E E ^NQ Y ^SN S T Y R V V -

1741 TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGG
 -----+-----+-----+-----+-----+-----+ 1800
 AGTCGCAGGAGTGGCAGGACGTGGTCCTGACCGACTTACCGTTCCTCATGTTACGTTCC
 S V L T V L H Q D W L N G K E Y K C ^NK V -

1801 TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGTGGGA
 -----+-----+-----+-----+-----+-----+ 1860
 AGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCGGTTTCCACCCT
 S N K A L P A P I E K ^NT I S K A K

1861 CCCGTGGGGTGCGAGGGCCACATGGACAGAGGCCGGCTCGGCCCACCCTCTGCCCTGAGA
 -----+-----+-----+-----+-----+-----+ 1920
 GGGCACCCACGCTCCCGGTGTACCTGTCTCCGCGCGAGCCGGGTGGGAGACGGGACTCT

1921 GTGACCGCTGTACCAACCTCTGTCTTACAGGGCAGCCCCGAGAACCACAGGTGTACACCC
 -----+-----+-----+-----+-----+-----+ 1980
 CACTGGCGACATGGTTGGAGACAGGATGTCCCGTCGGGGCTCTTGGTGTCCACATGTGGG
 G Q P R E P Q V Y T L -

1981 TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
 -----+-----+-----+-----+-----+-----+ 2040
 ACGGGGGTAGGGCCCTACTCGACTGGTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTC
 P P S R D E L T K N Q V S L T C L V K G -

Fig. 10D

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2041 GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAAC
-----+-----+-----+-----+-----+-----+ 2100
CGAAGATAGGGTCGCTGTAGCGGCACCTCACCTCTCGTTACCCGTCGGCCTCTTGTTGA
      F Y P S D I A V E W E S N G Q P E N N Y -

2101 ACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCA
-----+-----+-----+-----+-----+-----+ 2160
TGTTCTGGTGCGGAGGGCACGACCTGAGGCTGCCGAGGAAGAAGGAGATGTCGTTCGAGT
      K T T P P V L D S D G S F F L Y S K L T -

2161 CCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGG
-----+-----+-----+-----+-----+-----+ 2220
GGCACCTGTTCTCGTCCACCGTCGTCCCCCTTGAGAAGAGTACGAGGCACTACGTACTCC
      V D K S R W Q Q G N V F S C S V M H E A -

2221 CTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGCGAC
-----+-----+-----+-----+-----+-----+ 2280
GAGACGTGTTGGTGATGTGCGTCTTCTCGGAGAGGGACAGAGGCCCATTTACTCACGCTG
      L H N H Y T Q K S L S L S P G K *

2281 GGCCGGC
-----
CCGGCCG

```

Fig. 10E

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1  ATGGCGCTGT CCTGGGTTCT TACAGTCCTG AGCCTCCTAC CTCTGCTGGA
51  AGCCCAGATC CCATTGTGTG CCAACCTAGT ACCGGTGCCC ATCACCAACG
101 CCACCCTGGA CCAGATCACT GGCAAGTGGT TTTATATCGC ATCGGCCTTT
151 CGAAACGAGG AGTACAATAA GTCGGTTCAG GAGATCCAAG CAACCTTCTT
201 TTACTTCACC CCCAACAAGA CAGAGGACAC GATCTTTCTC AGAGAGTACC
251 AGACCCGACA GGACCAGTGC ATCTATAACA CCACCTACCT GAATGTCCAG
301 CGGGAAAATG GGACCATCTC CAGATACGTG GGAGGCCAAG AGCATTTTCG
351 TCACTTGCTG ATCCTCAGGG ACACCAAGAC CTACATGCTT GCTTTTGACG
401 TGAACGATGA GAAGAACTGG GGGCTGTCTG TCTATGCTGA CAAGCCAGAG
451 ACGACCAAGG AGCAACTGGG AGAGTTCTAC GAAGCTCTCG ACTGCTTGCG
501 CATTCCCAAG TCAGATGTCG TGTACACCGA TTGGAAAAAG GATAAGTGTG
551 AGCCACTGGA GAAGCAGCAC GAGAAGGAGA GGAAACAGGA GGAGGGGGAA
601 TCGGATCCCG AGGGTGAGTA CTAAGCTTCA GCGCTCCTGC CTGGACGCAT
651 CCCGGCTATG CAGCCCCAGT CCAGGGCAGC AAGGCAGGCC CCGTCTGCCT
701 CTTACCCCGG AGCCTCTGCC CGCCCCACTC ATGCTCAGGG AGAGGGTCTT
751 CTGGCTTTTT CCCAGGCTCT GGGCAGGCAC AGGCTAGGTG CCCCTAACCC
801 AGGCCCTGCA CACAAAGGGG CAGGTGCTGG GCTCAGACCT GCCAAGAGCC
851 ATATCCGGGA GGACCCTGCC CCTGACCTAA GCCCACCCEA AAGGCCAAAC
901 TCTCCACTCC CTCAGCTCGG ACACCTTCTC TCCTCCCAGA TTCCAGTAAC
951 TCCCAATCTT CTCTCTGCAG AGCCCAAATC TTGTGACAAA ACTCACACAT
1001 GCCCACC GTG CCCAGGTAAG CCAGCCCAGG CCTCGCCCTC CAGCTCAAGG
1051 CGGGACAGGT GCCCTAGAGT AGCCTGCATC CAGGGACAGG CCCCAGCCGG
1101 GTGCTGACAC GTCCACCTCC ATCTCTTCCT CAGCACCTGA ACTCCTGGGG
1151 GGACCGTCAG TCTTCCTCTT CCCCCAAAAA CCCAAGGACA CCCTCATGAT

```

Fig. 11A

1201 CTCCCGGACC CCTGAGGTCA CATGCGTGGT GGTGGACGTG AGCCACGAAG
 1251 ACCCTGAGGT CAAGTTCAAC TGGTACGTGG ACGGCGTGGA GGTGCATAAT
 1301 GCCAAGACAA AGCCGCGGGA GGAGCAGTAC AACAGCACGT ACCGGGTGGT
 1351 CAGCGTCCTC ACCGTCCTGC ACCAGGACTG GCTGAATGGC AAGGAGTACA
 1401 AGTGCAAGGT CTCCAACAAA GCCCTCCCAG CCCCCATCGA GAAAACCATC
 1451 TCCAAAGCCA AAGGTGGGAC CCGTGGGGTG CGAGGGCCAC ATGGACAGAG
 1501 GCCGGCTCGG CCCACCCTCT GCCCTGAGAG TGACCGCTGT ACCAACCTCT
 1551 GTCCTACAGG GCAGCCCCGA GAACCACAGG TGTACACCCT GCCCCATCC
 1601 CGGGATGAGC TGACCAAGAA CCAGGTCAGC CTGACCTGCC TGGTCAAAGG
 1651 CTTCTATCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT GGGCAGCCGG
 1701 AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA CGGCTCCTTC
 1751 TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGGAA
 1801 CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC
 1851 AGAAGAGCCT CTCCCTGTCT CCGGGTAAAT GAGTGCGACG GCCG

Fig. 11B

1 MALSWVLTVL SLLPLLEAQI PLCANLVPVP ITNATLDQIT GKWFYIASAF
 51 RNEEYNKSVQ EIQATFFYFT PNKTEDTIFL REYQTRQDQC IYNTTYLNVQ
 101 RENGTSRYV GGQEHFAHLL ILRDTKTYML AFDVNDEKNW GLSVYADKPE
 151 TTKEQLGEFY EALDCLRIPK SDVVYTDWKK DKCEPLEKQH EKERKQEEGE
 201 SDPEGEPKSC DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT
 251 CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH
 301 QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK
 351 NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL
 401 TVDKSRWQQG NVFSCSVMHE ALHNHYTQKS LSLSPGK*

Fig. 11C

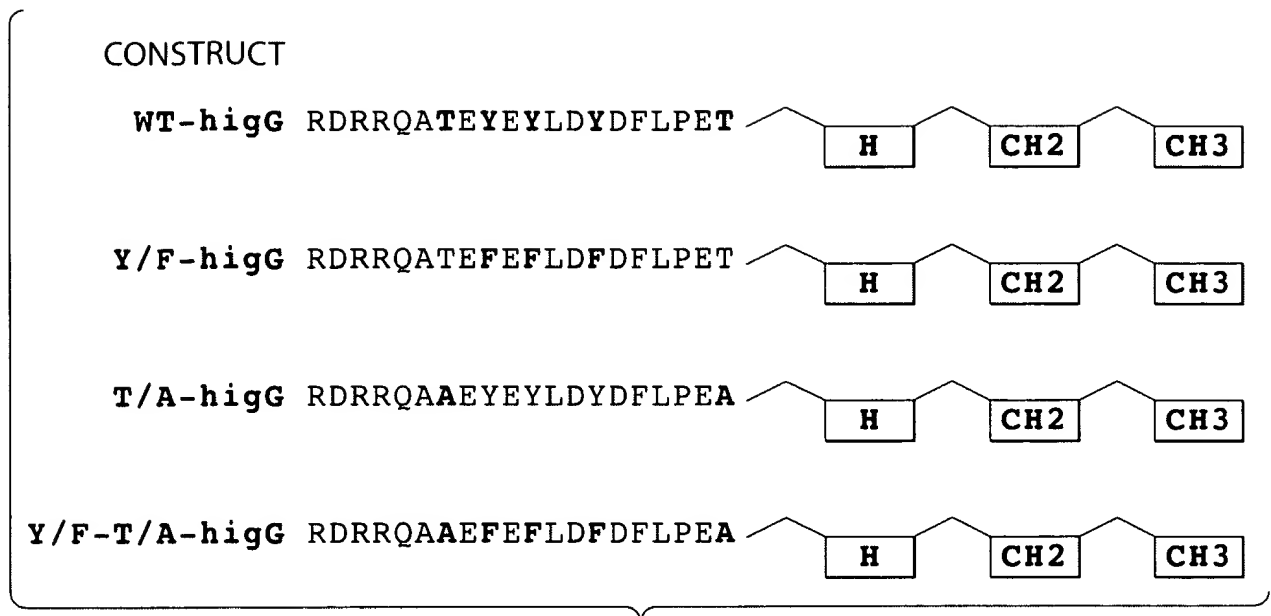


Fig. 12A

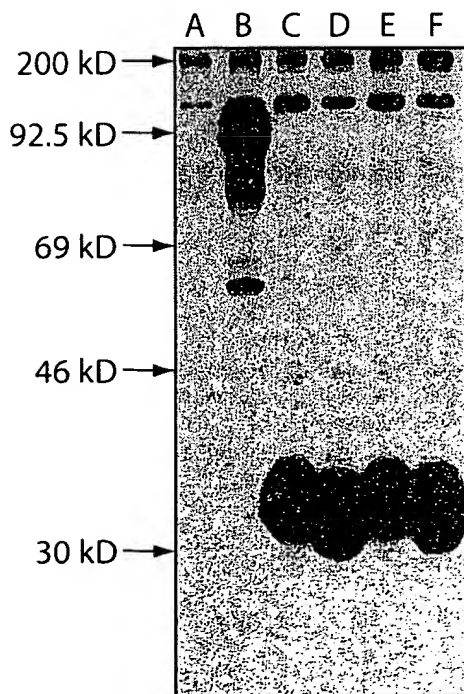


Fig. 12B

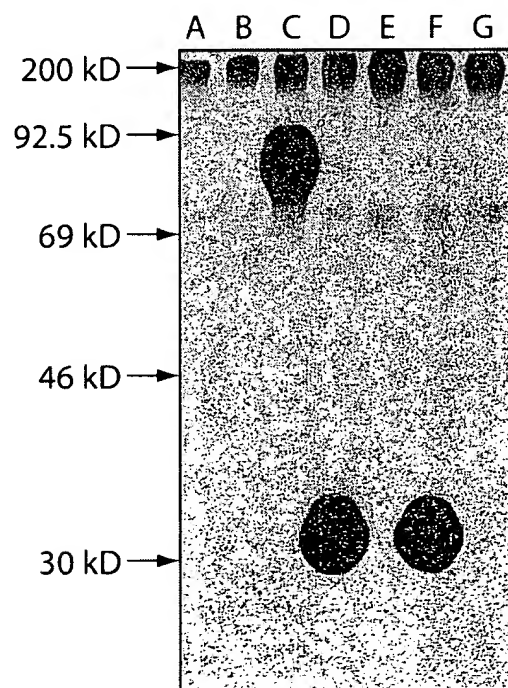


Fig. 12C

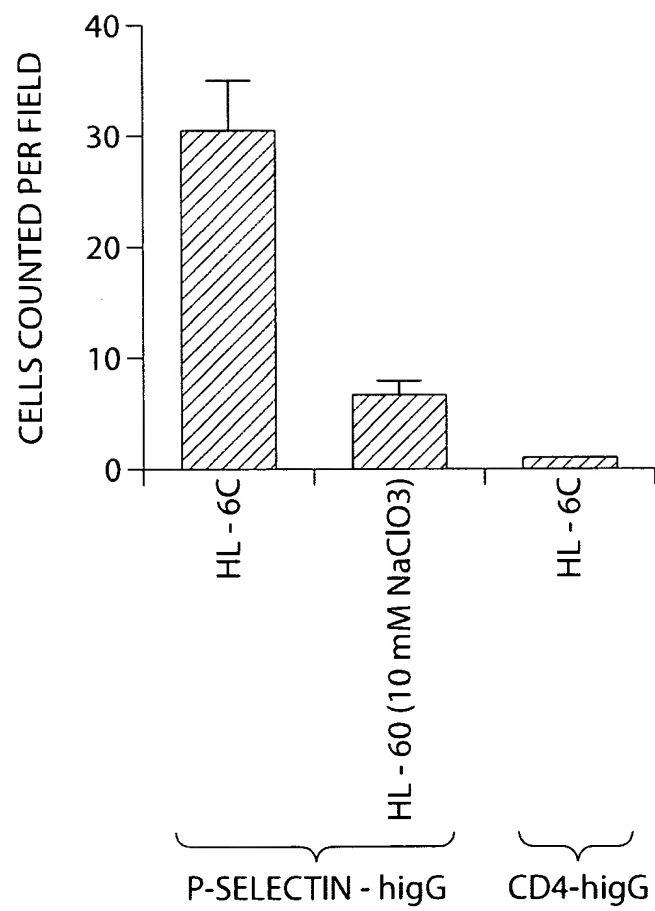


Fig. 13

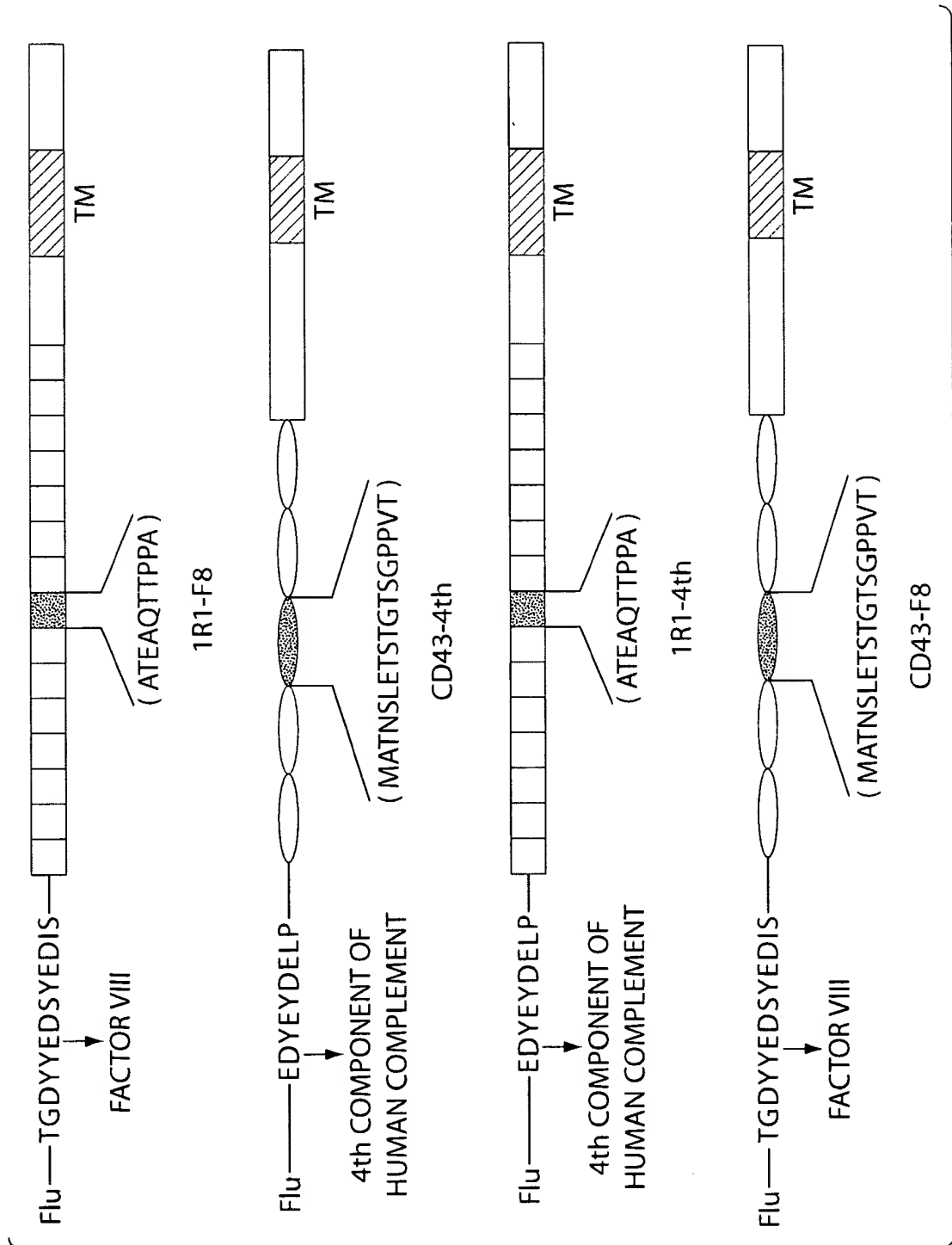


Fig. 14

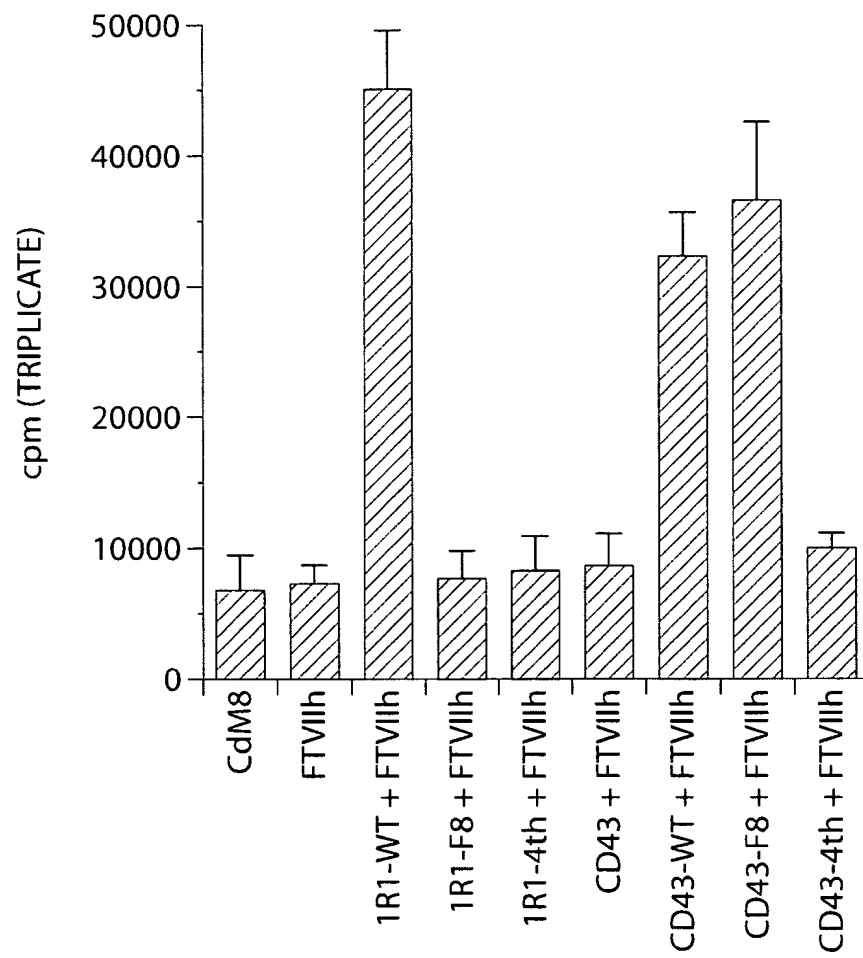


Fig. 15